

- 21 -

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANTS:

(A) NAME: SemBioSys Genetics Inc.  
(B) STREET: 2500 University Drive N.W.  
(C) CITY: Calgary  
(D) STATE: Alberta  
(E) COUNTRY: Canada  
(F) POSTAL CODE: T2N 1N4  
(G) TELEPHONE NO.: (403) 220-5161  
(H) TELEFAX NO.: (403) 220-0704

(A) NAME: van Rooijen, Gijs  
(B) STREET: 3223 Bearspaw Drive N.W.  
(C) CITY: Calgary  
(D) STATE: Alberta  
(E) COUNTRY: Canada  
(F) POSTAL CODE: T2L 1T1

(A) NAME: Alcantara, Joenel  
(B) STREET: 3 Castledale Place N.W.  
(C) CITY: Calgary  
(D) STATE: Alberta  
(E) COUNTRY: Canada  
(F) POSTAL CODE: T3J 1Y4

(A) NAME: Moloney, Maurice M.  
(B) STREET: 34 Edgebrook Cove, N.W.  
(C) CITY: Calgary  
(D) STATE: Alberta  
(E) COUNTRY: Canada  
(F) POSTAL CODE: T3A 5N5

(ii) TITLE OF INVENTION: Method for Cleavage of Fusion Proteins

(iii) NUMBER OF SEQUENCES: 4

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: BERESKIN & PARR  
(B) STREET: 40 King Street West  
(C) CITY: Toronto  
(D) STATE: Ontario  
(E) COUNTRY: Canada  
(F) ZIP: M5H 3Y2

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: PCT  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Gravelle, Micheline  
(B) REGISTRATION NUMBER: 40,261  
(C) REFERENCE/DOCKET NUMBER: 9369-54

- 22 -

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (416) 364-7311

(B) TELEFAX: (416) 361-1398

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1096 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1032

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG	TCC	CCT	ATA	CTA	GGT	TAT	TGG	AAA	ATT	AAG	GGC	CTT	GTG	CAA	CCC	48
Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro	
1				5				10						15		
ACT	CGA	CTT	CTT	TTG	GAA	TAT	CTT	GAA	GAA	AAA	TAT	GAA	GAG	CAT	TTG	96
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
			20					25					30			
TAT	GAG	CGC	GAT	GAA	GGT	GAT	AAA	TGG	CGA	AAC	AAA	AAG	TTT	GAA	TTG	144
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
		35					40					45				
GGT	TTG	GAG	TTT	CCC	AAT	CTT	CCT	TAT	TAT	ATT	GAT	GGT	GAT	GTT	AAA	192
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
	50					55					60					
TTA	ACA	CAG	TCT	ATG	GCC	ATC	ATA	CGT	TAT	ATA	GCT	GAC	AAG	CAC	AAC	240
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
65					70				75						80	
ATG	TTG	GGT	GGT	TGT	CCA	AAA	GAG	CGT	GCA	GAG	ATT	TCA	ATG	CTT	GAA	288
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
				85				90						95		
GGA	GCG	GTT	TTG	GAT	ATT	AGA	TAC	GGT	GTT	TCG	AGA	ATT	GCA	TAT	AGT	336
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
			100					105					110			
AAA	GAC	TTT	GAA	ACT	CTC	AAA	GTT	GAT	TTT	CTT	AGC	AAG	CTA	CCT	GAA	384
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
		115					120					125				
ATG	CTG	AAA	ATG	TTC	GAA	GAT	CGT	TTA	TGT	CAT	AAA	ACA	TAT	TTA	AAT	432
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
	130					135					140					
GGT	GAT	CAT	GTA	ACC	CAT	CCT	GAC	TTC	ATG	TTG	TAT	GAC	GCT	CTT	GAT	480
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
145					150					155					160	
GTT	GTT	TTA	TAC	ATG	GAC	CCA	ATG	TGC	CTG	GAT	GCG	TTC	CCA	AAA	TTA	528
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
				165					170					175		

- 23 -

GTT	TGT	TTT	AAA	AAA	CGT	ATT	GAA	GCT	ATC	CCA	CAA	ATT	GAT	AAG	TAC	576
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
			180					185					190			
TTG	AAA	TCC	AGC	AAG	TAT	ATA	GCA	TGG	CCT	TTG	CAG	GGC	TGG	CAA	GCC	624
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
		195					200					205				
ACG	TTT	GGT	GGT	GGC	GAC	CAT	CCT	CCA	AAA	TCG	GAT	CTG	GTT	CCG	CGT	672
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
	210					215					220					
GGA	TCC	CCG	AAT	TCC	CGG	GTC	GAC	TCG	AGC	GGC	CGC	GCT	GAG	ATC	ACC	720
Gly	Ser	Pro	Asn	Ser	Arg	Val	Asp	Ser	Ser	Gly	Arg	Ala	Glu	Ile	Thr	
225					230					235					240	
AGG	ATC	CCT	CTG	TAC	AAA	GGC	AAG	TCT	CTG	AGG	AAG	GCG	CTG	AAG	GAG	768
Arg	Ile	Pro	Leu	Tyr	Lys	Gly	Lys	Ser	Leu	Arg	Lys	Ala	Leu	Lys	Glu	
				245					250					255		
CAT	GGG	CTT	CTG	GAG	GAC	TTC	CTG	CAG	AAA	CAG	CAG	TAT	GGC	ATC	AGC	816
His	Gly	Leu	Leu	Glu	Asp	Phe	Leu	Gln	Lys	Gln	Gln	Tyr	Gly	Ile	Ser	
			260					265					270			
AGC	AAG	TAC	TCC	GGC	TTC	GTC	GTC	TAT	ACC	GAC	TGT	ACC	GAG	TCC	GGT	864
Ser	Lys	Tyr	Ser	Gly	Phe	Val	Val	Tyr	Thr	Asp	Cys	Thr	Glu	Ser	Gly	
		275					280					285				
CAG	AAC	CTC	TGT	CTC	TGT	GAG	GGT	TCC	AAC	GTC	TGT	GGT	CAG	GGT	AAC	912
Gln	Asn	Leu	Cys	Leu	Cys	Glu	Gly	Ser	Asn	Val	Cys	Gly	Gln	Gly	Asn	
	290					295					300					
AAG	TGT	ATC	CTC	GGT	TCC	GAC	GGT	GAG	AAG	AAC	CAG	TGT	GTC	ACC	GGT	960
Lys	Cys	Ile	Leu	Gly	Ser	Asp	Gly	Glu	Lys	Asn	Gln	Cys	Val	Thr	Gly	
305					310					315					320	
GAG	GGA	ACC	CCA	AAG	CCA	CAG	TCC	CAC	AAC	GAC	GGT	GAC	TTT	GAG	GAG	1008
Glu	Gly	Thr	Pro	Lys	Pro	Gln	Ser	His	Asn	Asp	Gly	Asp	Phe	Glu	Glu	
				325					330					335		
ATC	CCA	GAG	GAG	TAT	CTC	CAG	TAA	AGATCTAAGC	TTGCTGCTGC	TATCGAATTC						1062
Ile	Pro	Glu	Glu	Tyr	Leu	Gln	*									
			340													
CTGCAGCCCCG	GGGGATCCAC	TAGTTCTAGA	GCGG													1096

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45

- 24 -

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Asn Ser Arg Val Asp Ser Ser Gly Arg Ala Glu Ile Thr  
 225 230 235 240  
 Arg Ile Pro Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu  
 245 250 255  
 His Gly Leu Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser  
 260 265 270  
 Ser Lys Tyr Ser Gly Phe Val Val Tyr Thr Asp Cys Thr Glu Ser Gly  
 275 280 285  
 Gln Asn Leu Cys Leu Cys Glu Gly Ser Asn Val Cys Gly Gln Gly Asn  
 290 295 300  
 Lys Cys Ile Leu Gly Ser Asp Gly Glu Lys Asn Gln Cys Val Thr Gly  
 305 310 315 320  
 Glu Gly Thr Pro Lys Pro Gln Ser His Asn Asp Gly Asp Phe Glu Glu  
 325 330 335  
 Ile Pro Glu Glu Tyr Leu Gln \*  
 340

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- 25 -

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..819

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG	CGG	GGT	TCT	CAT	CAT	CAT	CAT	CAT	CAT	GGT	ATG	GCT	AGC	ATG	ACT	48
Met	Arg	Gly	Ser	His	His	His	His	His	His	Gly	Met	Ala	Ser	Met	Thr	
1				5					10					15		
GGT	GGA	CAG	CAA	ATG	GGT	CGG	GAT	CTG	TAC	GAC	GAT	GAC	GAT	AAG	GAT	96
Gly	Gly	Gln	Gln	Met	Gly	Arg	Asp	Leu	Tyr	Asp	Asp	Asp	Asp	Lys	Asp	
			20					25						30		
CCG	AGC	TCG	AGA	TCT	GCA	GAA	ATC	GGA	TCC	GCT	GAG	ATC	ACC	AGG	ATC	144
Pro	Ser	Ser	Arg	Ser	Ala	Glu	Ile	Gly	Ser	Ala	Glu	Ile	Thr	Arg	Ile	
		35					40					45				
CCT	CTG	TAC	AAA	GGC	AAG	TCT	CTG	AGG	AAG	GCG	CTG	AAG	GAG	CAT	GGG	192
Pro	Leu	Tyr	Lys	Gly	Lys	Ser	Leu	Arg	Lys	Ala	Leu	Lys	Glu	His	Gly	
	50					55					60					
CTT	CTG	GAG	GAC	TTC	CTG	CAG	AAA	CAG	CAG	TAT	GGC	ATC	AGC	AGC	AAG	240
Leu	Leu	Glu	Asp	Phe	Leu	Gln	Lys	Gln	Gln	Tyr	Gly	Ile	Ser	Ser	Lys	
	65				70					75					80	
TAC	TCC	GGC	TTC	TCA	GAC	AAC	CAG	CGG	CTC	TTC	AAT	AAT	GCA	GTC	ATT	288
Tyr	Ser	Gly	Phe	Ser	Asp	Asn	Gln	Arg	Leu	Phe	Asn	Asn	Ala	Val	Ile	
				85					90					95		
CGT	GTA	CAA	CAC	CTG	CAC	CAG	CTG	GCT	GCA	AAA	ATG	ATT	AAC	GAC	TTT	336
Arg	Val	Gln	His	Leu	His	Gln	Leu	Ala	Ala	Lys	Met	Ile	Asn	Asp	Phe	
			100					105					110			
GAG	GAC	AGC	CTG	TTG	CCT	GAG	GAA	CGC	AGA	CAG	CTG	AGT	AAA	ATC	TTC	384
Glu	Asp	Ser	Leu	Leu	Pro	Glu	Glu	Arg	Arg	Gln	Leu	Ser	Lys	Ile	Phe	
		115					120					125				
CCT	CTG	TCT	TTC	TGC	AAT	TCT	GAC	TAC	ATT	GAG	GCG	CCT	GCT	GGA	AAA	432
Pro	Leu	Ser	Phe	Cys	Asn	Ser	Asp	Tyr	Ile	Glu	Ala	Pro	Ala	Gly	Lys	
	130					135					140					
GAT	GAA	ACA	CAG	AAG	AGC	TCT	ATG	CTG	AAG	CTT	CTT	CGC	ATC	TCT	TTT	480
Asp	Glu	Thr	Gln	Lys	Ser	Ser	Met	Leu	Lys	Leu	Leu	Arg	Ile	Ser	Phe	
	145				150					155					160	
CAC	CTC	ATT	GAG	TCC	TGG	GAG	TTC	CCA	AGC	CAG	TCC	CTG	AGC	GGA	ACC	528
His	Leu	Ile	Glu	Ser	Trp	Glu	Phe	Pro	Ser	Gln	Ser	Leu	Ser	Gly	Thr	
				165					170					175		
GTC	TCA	AAC	AGC	CTG	ACC	GTA	GGG	AAC	CCC	AAC	CAG	CTC	ACT	GAG	AAG	576
Val	Ser	Asn	Ser	Leu	Thr	Val	Gly	Asn	Pro	Asn	Gln	Leu	Thr	Glu	Lys	
			180					185					190			
CTG	GCC	GAC	TTG	AAA	ATG	GGC	ATC	AGT	GTG	CTC	ATC	CAG	GCA	TGT	CTC	624
Leu	Ala	Asp	Leu	Lys	Met	Gly	Ile	Ser	Val	Leu	Ile	Gln	Ala	Cys	Leu	
		195					200					205				
GAT	GGT	CAA	CCA	AAC	ATG	GAT	GAT	AAC	GAC	TCC	TTG	CCG	CTG	CCT	TTT	672
Asp	Gly	Gln	Pro	Asn	Met	Asp	Asp	Asn	Asp	Ser	Leu	Pro	Leu	Pro	Phe	
	210					215					220					
GAG	GAC	TTC	TAC	TTG	ACC	ATG	GGG	GAG	AAC	AAC	CTC	AGA	GAG	AGC	TTT	720
Glu	Asp	Phe	Tyr	Leu	Thr	Met	Gly	Glu	Asn	Asn	Leu	Arg	Glu	Ser	Phe	

- 26 -

225		230		235		240	
CGT CTG CTG GCT TGC TTC AAG AAG GAC ATG CAC AAA GTC GAG ACC TAC							768
Arg Leu Leu Ala Cys Phe Lys Lys Asp Met His Lys Val Glu Thr Tyr							
		245		250		255	
TTG AGG GTT GCA AAT TGC AGG AGA TCC CTG GAT TCC AAC TGC ACC CTG							816
Leu Arg Val Ala Asn Cys Arg Arg Ser Leu Asp Ser Asn Cys Thr Leu							
		260		265		270	
TAG							819
*							

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Arg Gly Ser His His His His His Gly Met Ala Ser Met Thr
 1              5              10              15
Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
      20              25              30
Pro Ser Ser Arg Ser Ala Glu Ile Gly Ser Ala Glu Ile Thr Arg Ile
      35              40              45
Pro Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly
      50              55              60
Leu Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys
      65              70              75              80
Tyr Ser Gly Phe Ser Asp Asn Gln Arg Leu Phe Asn Asn Ala Val Ile
      85              90              95
Arg Val Gln His Leu His Gln Leu Ala Ala Lys Met Ile Asn Asp Phe
      100             105             110
Glu Asp Ser Leu Leu Pro Glu Glu Arg Arg Gln Leu Ser Lys Ile Phe
      115             120             125
Pro Leu Ser Phe Cys Asn Ser Asp Tyr Ile Glu Ala Pro Ala Gly Lys
      130             135             140
Asp Glu Thr Gln Lys Ser Ser Met Leu Lys Leu Leu Arg Ile Ser Phe
      145             150             155             160
His Leu Ile Glu Ser Trp Glu Phe Pro Ser Gln Ser Leu Ser Gly Thr
      165             170             175
Val Ser Asn Ser Leu Thr Val Gly Asn Pro Asn Gln Leu Thr Glu Lys
      180             185             190
Leu Ala Asp Leu Lys Met Gly Ile Ser Val Leu Ile Gln Ala Cys Leu
      195             200             205
Asp Gly Gln Pro Asn Met Asp Asp Asn Asp Ser Leu Pro Leu Pro Phe

```

- 27 -

210					215					220					
Glu	Asp	Phe	Tyr	Leu	Thr	Met	Gly	Glu	Asn	Asn	Leu	Arg	Glu	Ser	Phe
225					230					235					240
Arg	Leu	Leu	Ala	Cys	Phe	Lys	Lys	Asp	Met	His	Lys	Val	Glu	Thr	Tyr
				245					250					255	
Leu	Arg	Val	Ala	Asn	Cys	Arg	Arg	Ser	Leu	Asp	Ser	Asn	Cys	Thr	Leu
			260					265					270		

\*